Accuracy of genomic prediction within and across populations for nematode resistance and body weight traits in sheep

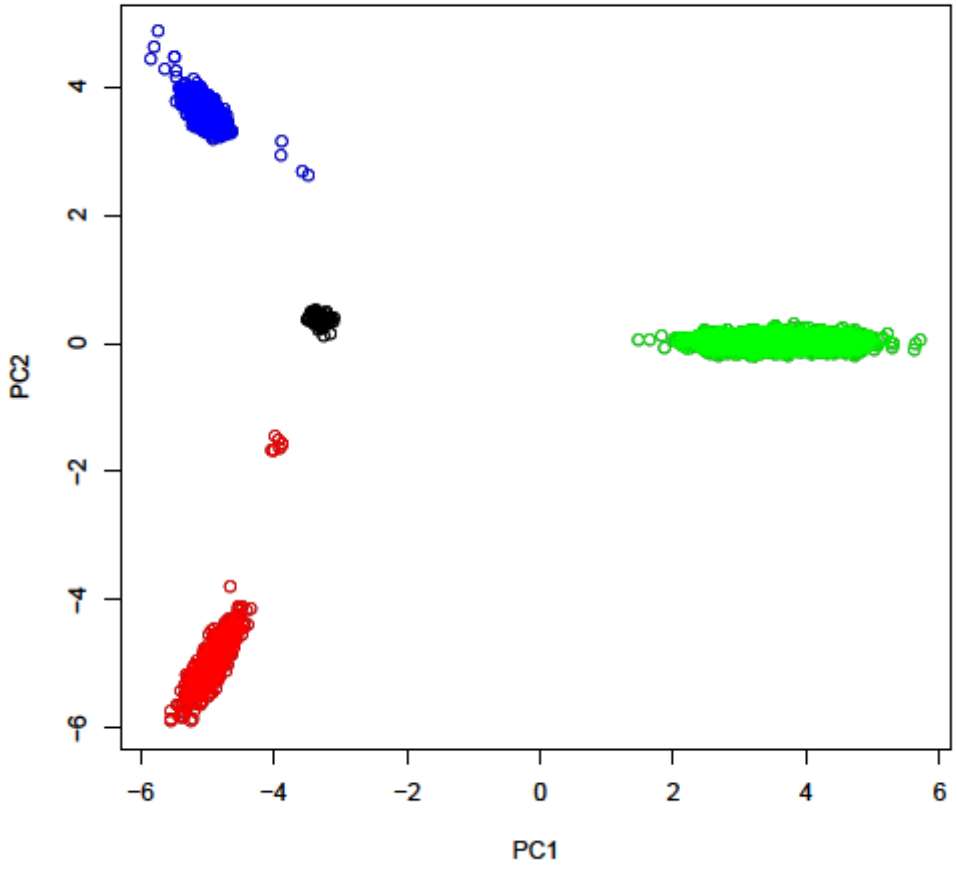
Supplementary File 1: Quality control (QC) measures, specific for each population.

For the Scottish Blackface and the British Texel, the QC removed the SNPs with a minor-allele frequency < 0.02 or a call rate < 95%. Deviation from Hardy–Weinberg equilibrium was not considered as a method for excluding SNPs. Furthermore, markers on the sex chromosome and markers unmapped were removed from the analysis (Riggio et al. 2013, Heredity 110: 420-429).

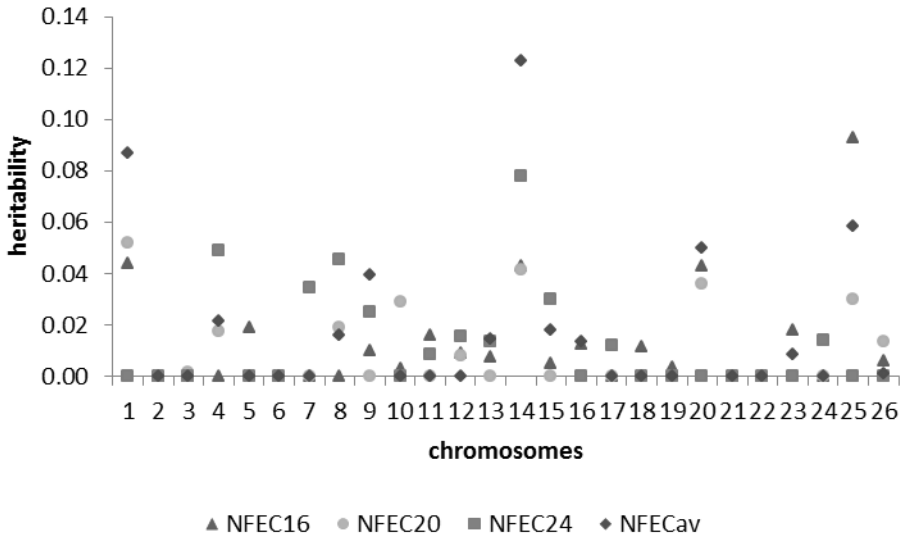
For the Martinik Black-Belly x Romane backcross, individuals with a call rate below 98% were discarded, and a 99.9% technical reliability was established by duplicated genotyping in 50 animals. In addition, Mendelian inconsistencies (i.e., no allele shared in common between a progeny and its sire for a given SNP) were checked. Intrinsic SNP quality criteria were also considered. Useless SNP that had been eliminated in the frame of the sheep HAPMAP project (i.e., SNP that Illumina annotated as abnormal; SNP with minor allele frequencies equal to 0; SNP that displayed discordant genotypes between experiments; or SNP showing Mendelian inconsistencies within the International Mapping Flock) were discarded (J. W. Kijas, personal communication). SNP with a call rate < 97% were removed. A minor allele frequency < 1% was applied. A test for Hardy-Weinberg disequilibrium was also considered to eliminate SNP with abnormal behavior (P < 10–6) in purebred populations, and these SNPs were also eliminated from the backcross genotype data. Furthermore, SNPs for which more heterozygotes than expected (i.e., 50% for a heterozygous sire) were counted, or SNPs with too great a recombination rate were not included in the QTL analysis. Sex chromosomes were not considered for analysis (Salle et al. 2012, JAS 90:4690-4705).

For the Sarda x Lacaune backcross, individuals with a proportion of genotypes missing > 10% were excluded. All SNPs which could not be mapped or were on the sex chromosome were excluded from the data set. The SNPs with call rate < 95% and minor allele frequency < 1% were also excluded. Due to the family structure of the population, deviation from Hardy–Weinberg equilibrium was not considered.

Supplementary Figure S1: Plot of principal components (PC) 1 and 2 for the four populations considered. Coloured by population, with red being the Scottish Blackface, blue the Martinik Black-Belly x Romane backcross, green the Sarda x Lacaune backcross, and black the British Texel.



Supplementary Figure S2: Heritability estimates for all Nematodirus FEC traits fitting simultaneously one chromosome and the whole genomic relationship matrix.



Supplementary Table S1: Heritability estimates (± s.e.) when fitting only the pedigree or genomic relationship matrix, and when fitting simultaneously the pedigree and genomic relationship matrices, for nematode resistance indicator traits.

	Pedigree Matrix only	**Genomic Matrix only**	**Fitting Both Pedigree and Genomic Relationship matrices**	
	h^2 ± s.e.	**h^2 ± s.e.**	**h^2_{ped} ± s.e.**	**h^2_{gen} ± s.e.**
IgA	0.27 ± 0.09	0.30 ± 0.02	0.00 ± 0.00	0.30 ± 0.02
SFEC16	0.32 ± 0.12	0.16 ± 0.06	0.12 ± 0.12	0.12 ± 0.07
SFEC20	0.15 ±0.08	0.11 ± 0.05	0.12 ± 0.07	0.00 ± 0.00
SFEC24	0.21 ± 0.10	0.12 ± 0.05	0.12 ± 0.10	0.05 ± 0.07
NFEC16	0.10 ± 0.06	0.04 ± 0.04	0.07 ± 0.06	0.00 ± 0.00
NFEC20	0.16 ± 0.07	0.20 ± 0.05	0.00 ± 0.00	0.19 ± 0.06
NFEC24	0.12 ± 0.06	0.11 ± 0.05	0.02 ± 0.07	0.10 ± 0.06
SFEC_av	0.38 ± 0.11	0.22 ± 0.04	0.14 ± 0.11	0.19 ± 0.06
NFEC_av	0.29 ± 0.09	0.27 ± 0.03	0.09 ± 0.09	0.27 ± 0.04

IgA: Immunoglobulin-A; SFEC16, SFEC20, and SFEC24: faecal egg count at 16, 20 and 24 weeks for *Strongyles*; NFEC16, NFEC20, NFEC24: faecal egg count at 16, 20 and 24 weeks for *Nematodirus*; SFEC_av, NFEC_av: average animal effected for *Strongyles* and *Nematodirus* faecal egg count